AMENDMENTS TO THE CLAIMS

1.-37. (Canceled)

38. (Currently amended) The method of claim [[36]] 111 wherein said nucleic acid target is RNA.

39. (Currently amended) The method of claim [[38]] 111 wherein said nucleic acid target comprises RNA ~~includes~~ and one or more deoxynucleotides at preselected locations ~~thereof~~.

40.-94. (Canceled)

95. (Currently amended) The method of claim [[36]] 111, wherein ~~said compound~~ each member of said mixture of compounds is an oligonucleotide.

96. (Canceled)

97. (Currently amended) The method of claim [[36]] 111, wherein ~~said compound~~ each member of said mixture of compounds is a small molecule.

98. (Previously Presented) The method of claim 38, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

99. (Currently amended) The method of claim [[41]] 112, wherein ~~said compound~~ each member of said mixture of compounds is an oligonucleotide.

100. (Canceled)

101. (Currently amended) The method of claim [[41]] 112, wherein said nucleic acid target is RNA.

102. (Canceled)

103. (Previously Presented) The method of claim 101, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

104. (Currently amended) The method of claim [[41]] 112, wherein ~~said compound~~ each member of said mixture of compounds is a small molecule.

105.-108. (Canceled)

109. (Previously presented) The method of claim 38, wherein said RNA comprises a molecular interaction site.

110. (Previously presented) The method of claim 101, wherein said RNA comprises a molecular interaction site.

111. (New) A method comprising

(a) selecting a nucleic acid target comprising at least one loop, bulge, kink, stem structure, or mismatched base pair;

(b) forming a complex comprising a standard binding compound and said nucleic acid target, wherein the complex has a known ion abundance and mass to charge ratio;

(c) combining with said complex a mixture of compounds under competitive binding conditions;

(d) subjecting said combination to mass spectrometry;

(e) collecting mass spectral data for said combination, wherein said mass spectral data provides an ion abundance and mass to charge ratio for a plurality of ions;

(f) comparing at least one mass to charge ratio obtained in step (e) to the known mass to charge ratio of the complex to determine whether binding of one or more members of said mixture of compounds to the nucleic acid target has occurred;

(g) calculating the mass of said one or more members to determine the identity of said one or more members; and

(h) comparing the ion abundance of said one or more members to the known ion abundance of the complex to determine a relative dissociation constant for said member, thereby determining binding affinity of said member for said nucleic acid target.

112. (New) A method comprising

(a) forming a complex of a nucleic acid target and a standard binding compound, wherein the nucleic acid target comprises at least one loop, bulge, kink, stem structure, or mismatched base pair;

(b) subjecting said complex to mass spectrometry;

(c) collecting mass spectral data for said complex, wherein the mass spectral data provides an ion abundance and a mass to charge ratio for an ion of the complex;

(d) combining said complex with a mixture of compounds under competitive binding conditions;

(e) subjecting said combination to mass spectrometry;

(f) collecting mass spectral data for said combination, wherein said mass spectral data provides an ion abundance and mass to charge ratio for one or more of a plurality of ions;

(g) comparing the mass to charge ratio collected in steps (c) and (f), to determine whether binding of one or more members of the mixture of compounds to the nucleic acid target has occurred;

(h) calculating the mass of said one or more members to determine the identity of said one or more members; and

(i) comparing the ion abundance of said one or more members to the ion abundance of said complex to determine a relative dissociation constant for said one or more members, thereby determining binding affinity of said member for said nucleic acid target.